

papiss.res

Tue Dec 4 10:02:55 2001

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CDS
3255..3581
/gene="E4"
/note="3255 is position of first start codon in ORF E4;
putative"
/codon_start=1
/protein_id="AAA6931.1"
/db_xref="GI:496197"
/translation="MVPVPOIAAATTTLLIPVIAFVAVLILILISDFVYT
IQQPAPRTACRRRLSEHVDPLTPCWPMSDPTVQSTSLITTSIKESGTV
TVOIRL"
3871..4146
/gene="E5A"
3871..4146
/gene="E5B"
/note="3871 is position of first start codon in ORF E5A;
putative"
/codon_start=1
/protein_id="AAA6932.1"
/db_xref="GI:496198"
/translation="MEVVPVQIAAATTTLLIPVIAFVAVLILILISDFVYT
SVVLTLLVLLMLLTPLQFFLLTLCVCFPAFYHIYVQOQ"
4146..4370
/gene="E5B"
4146..4370
/gene="E5B"
/note="4146 is position of first start codon in ORF E5B;
putative"
/codon_start=1
/protein_id="AAA6933.1"
/db_xref="GI:496199"
/translation="MVLTCILNDGDTPLFLMFAFVAVLILILILHRAVHGTEKT
KCAKCKSNRTYDVYVMSHGNDIVYIN"
4371..4376
/note="putative"
4417..5784
/gene="L2"
4417..5784
/gene="L2"
/note="4417 is position of first start codon in ORF L2;
putative"
/codon_start=1
/product="minor capsid protein"
/protein_id="AAA6934.1"
/db_xref="GI:496200"
/translation="MKPRARRRRKASATQLYQCKANGCPDVIVKVEHTTIADQIL
KWSLGVTFQGLGIGTAGSGRAGYIFLGSSPPKATLGGPAPRVVLEPPVAPSDPS
IVSLIESALINAGAPVPPVPGGFTITSESTPAILDVTNNHTTSVFNPPFT
EPVLIQPPVPAASHILISAPITISOVEDIPDTEFVSSDSGPTSSPLRAPFR
PRVGLYRALQOVQVDPAPLSTPORLTVDMRYEGEDVLOLTHESINAADETEL
DIILHRAPAITSRGLVRFKSRIGORSMWTRGCHIGARHIFQDISPVTOAADETEL
HPLVAANDTEFIYAEPDEFIDPVPVQHSYLOSILSTENPLSQSMGNTVPLSLPSPM
FVQSGPDTFTFASMGTPSPVTPALPTGPVITTSDFLHPTWYFARRRRKRIPLF
TDVAA"
4545..4551
/gene="L2"
/note="putative"
5771..7276
/gene="L1"
5771..7276
/gene="L1"
/note="5771 is position of first start codon in ORF L1;
putative"
/codon_start=1
/product="major capsid protein"
/protein_id="AAA6935.1"
/db_xref="GI:496201"
/translation="MMPSPDSVTVYPPPNPVSKYVATDAVYKRTNIFYHASSRLLAV
GHPYISIKYKNTKTVYKVSQYRFRVVLPPNKFALPDSLDPDTPFORLWMACTGL
EYGRGQPLGVSGHPLNKYDDVENSQYVGNPGQDNKRVNVMGADYKOTOLCVGCAV
PLGEHMGKGTCCSNTSYONGDCPLLELTSVIOGDMDVTGAMNPAIDLOTNKSQVP
LDICGTVCYKPDYLOMAAADPYGRDLFPYLKEDQMFARHFFNAGTGVGPRVDDLLVKG
GNNRSSVASIYVHTPSSGLVSSPAOLFKNKPYWLQKAGHNGNIGMHLFVTVYDDTF
RSTNMTLCASVSKSATYNTSDIKREYMRHVEFDLPFLQICSTITLSAEYMAIYIHMPN

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5'UTR
repeat_region
repeat_region
repeat_region
polyA_signal
protein_bind
polyA_signal
protein_bind
BASE COUNT 2406 a 1519 c 1736 g 2270 t
ORIGIN
PPH1 length: 7931 November 28, 2001 14:10 Type: N Check: 3689
Found using 'papiss' (pappu445.key)

...
669 CTTTAAACAACATTACCAATACTGACCTGTGCTGTGATGTGACAGACAGCTCGAC
729 TGGTTGTGAGTGCACAGCGAGACATGCACACTACAGACCTT
...

-- Search Statistics --
Times: CPU 00:00:00.03 Total elapsed 00:00:01.00
Number of sequences searched: 6
Number of sequence hits: 1
Number of separate matches: 1
Number of sequence hits saved: 0

```

> 0 <
0/10 Intelligenetics
> 0 <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "papis" --

Selected search type is key against sequence data banks or files.
Selected scope is Sequence.

Selected sequence key from "papu445.key":

papis (NA) ID papis NA preliminary pattern

1 followed by
2 a or g
2 a or g
2 cg
2 c or t
2 c or t
2 cg

Selected files:

File : hpvcomplete.seq

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	File Options:
Find non-matching hits only	No	Indirect file
Report key used	Yes	Sequence or key file
Note position of hit	Yes	List of hits
Display full annotations	Yes	Hit display
Sequence context	50	Name and annotations

No
No
Yes
Yes
Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

1 match found in sequence:

pap11 : TOIG of: pap11 check: 3689 from: 1 to: 7931
(from "hpvcomplete.seq")
TOIG of: pap11 check: 3689 from: 1 to: 7931

LOCUS PAP11 7931 bp DNA Circular VRL 02-JUN-1994

DEFINITION Human papillomavirus type 11 (HPV-11) complete genome.

ACCESSION M4119.1 GI:333026

VERSION M4119.1 GI:333026

KEYWORDS complete genome.

SOURCE Human laryngeal papillomavirus type 11 DNA.

ORGANISM Human papillomavirus type 11

REFERENCE 1 (bases 1 to 7931)
Papillomavirus

AUTHORS Dartmann K., Schwarz E., Gissmann L. and Zur Hausen H.

TITLE The nucleotide sequence and genome organization of human papilloma

JOURNAL Virology 151, 124-130 (1986)

MEDLINE 86181601

COMMENT ORF 11 is assumed to encode the major structural protein.

FEATURES location/Qualifiers

1..7931

/organism="Human papillomavirus type 11"

/db_xref="taxon:10580"

/note="putative"

/note="putative"

/function="gene transcription"

protein_bind
50..61
/bound_moiety="E2"

/note="putative"

/function="gene transcription"

/bound_moiety="E2"

/note="putative"

102..554
/gene="E6"

102..554
/gene="E6"

/note="102 is position of first start codon in ORF E6;

putative"

/codon_start=1

/product="transforming protein"

/protein_id="AAA46927.1"

/db_xref="GI:496193"

/translation="MESKDASTATSIDOLCTENLSLITLQICVCRNALTTATY

AVAKNLKVVWNRDPPFAACACCELECKGIRHFNFAAAPTVEETEDILKYL

RCYLCHRPICIEIKLHILGKARFIKLNKNGKRLCHWTCEMLP"

530..826
/gene="E7"

530..826
/gene="E7"

/note="530 is position of first start codon in ORF E7;

putative"

/codon_start=1

/product="transforming protein"

/protein_id="AAA46928.1"

/db_xref="GI:496194"

/translation="MGRVLTKDIVLDIQPPDPVGLCYEQLEDSEDEVDKDKD

ADPLVGHVQILTCGCCDSNVLVVECTGDRIQLDLILGLTNIVPICAPK"

832..2781
/gene="E1"

832..2781
/gene="E1"

/note="832 is position of first start codon in ORF E1;

putative"

/codon_start=1

/product="replication protein"

/protein_id="AAA46929.1"

/db_xref="GI:496195"

/translation="MADSCGENSGCTGFWVEAIVBHTTGTQISEDEFEEDDS

ESLISRLDAIKLTTOPKKVRRLFEFRELDTSGYSEVFAATQVEKHPENGDC

QERDGRDIEGEVHEHREAVDSTREHADSGLLELCKDIASTHKGKFCGL

SEVDLIRPEKSDRTTCADNYVAGFGIHNHJLEPKTIGSVRALYMLTNGKFCGL

LVLIRFKVNRKRCVANTLSTLNLINPEHMLLEPKTIGSVRALYMLTNGKFCGL

FLNSMOKAKYKDCALMCRHAKHAKKMSIKOWIKGTIVDSVGMKPIYPLRHO

NIEFTPLSLKLMHGTGPKKNCIAIVGPDGSCGKMSLIKPLAGTIVISYNSCH

FMLOPLDANKVALLDATOPCWYMDTYMRNLDSGNSIDRKRLATLTKCPPLVT

SNIDISKEEKYKLHRSVTFTEFPNPFEDKNGNAVELSDAMKCFERLSSDIE

2723..3826
/gene="E2"

2723..3826
/gene="E2"

/note="2723 is position of first start codon in ORF E2;

putative"

/codon_start=1

/product="regulatory protein"

/protein_id="AAA46930.1"

/db_xref="GI:496196"

/translation="MEAIARLDACDQLELEYEENSIDIKHIMHKCTRISSVLH

LTPKRCFKRGKNGVVEKEDGCEBNVMEVWVTHIYLDNDNSWKVPSVADGIYV

CGQFKTYIVNFKENAKGTSTNHMEVCGSVICSPASVSTREVSIAPTTYTPAQ

TTAPTVACTTDEGVSAPPRKARAGPSTNNTLCVANSISVDSTINNTVDNKKHOR

NCHSAANPVOLOGDSNCLCFRYRLNDKIKHLFELASSTWMASSPEAPHKAIATVL

3255..3581
/gene="E4"